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☐ 1: P53909. Adenosine deamina...[gi:1703166]

[Related Sequences](#), [PubMed](#), [Taxonomy](#), [BLINK](#), [LinkOut](#)

LOCUS ADA_YEAST 347 aa linear PLN 16-OCT-2001
 DEFINITION Adenosine deaminase (Adenosine aminohydrolase).
 ACCESSION P53909
 PID g1703166
 VERSION P53909 GI:1703166
 DBSOURCE swissprot: locus ADA_YEAST, accession P53909;
 class: standard.
 created: Oct 1, 1996.
 sequence updated: Oct 1, 1996.
 annotation updated: Oct 16, 2001.
 xrefs: gi: gi: 861113, gi: gi: 854497, gi: gi: 1302088, gi: gi: 1302089
 xrefs (non-sequence databases): SGD S0005085, InterPro IPR001365, Pfam PF00962, PROSITE PS00485
 KEYWORDS Hydrolase; Nucleotide metabolism.
 SOURCE baker's yeast.
 ORGANISM Saccharomyces cerevisiae
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 REFERENCE 1 (residues 1 to 347)
 AUTHORS Mallet, L., Bussereau, F. and Jacquet, M.
 TITLE A 43.5 kb segment of yeast chromosome XIV, which contains MFA2, MEP2, CAP/SRV2, NAM9, FKB1/FPR1/RBP1, MOM22 and CPT1, predicts an adenosine deaminase gene and 14 new open reading frames
 JOURNAL Yeast 11 (12), 1195-1209 (1995)
 MEDLINE 96109932
 REMARK SEQUENCE FROM N.A.
 STRAIN=S288C

COMMENT

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[CATALYTIC ACTIVITY] ADENOSINE + H(2)O = INOSINE + NH(3) (ALSO ACTS ON DEOXYADENOSINE).
 [SIMILARITY] BELONGS TO THE ADENOSINE AND AMP DEAMINASES FAMILY.

FEATURES

source

Location/Qualifiers

1..347

/organism="Saccharomyces cerevisiae"

/db_xref="taxon:4932"

1..347

Protein

1..347

/product="Adenosine deaminase"

/EC_number="3.5.4.4"

Site

204

/site_type="active"

/note="POTENTIAL."

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Site      252
           /site_type="active"
           /note="POTENTIAL."
Site      285
           /site_type="active"
           /note="POTENTIAL."
Site      286
           /site_type="active"
           /note="POTENTIAL."
ORIGIN
    1 mvsveflqel pkcehhhlhle gtlepdlfp lakrndiilp egfpksveel nekykkfrdl
   61 qdfldyyyig tnvliseqdf fdlawayfkk vkhqglvhae vfydpgshts rgisietvbk
  121 gfqracdkaf sefgitskli mcllrhiepe eclktieeat pfikdgtisa lgldsaeckpf
  181 pphlfvecyg kaaslnkdlk ltahageegp aqfvsdaldl lqvtridhgi nsqydeelll
  241 rlsrdqtmlt icplsnvklq vvqsvselp1 qkfldrdrvpf slnsddpayf ggyildvytq
  301 vskdfphwdh etwgriakna ikgswcddkr knllsrnde vvtkysh
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☐ 1: AAA62126. AMP deaminase iso...

[gi:644509]

 Nucleotide, Related Sequences, Taxonomy, BLINK,
LinkOut

LOCUS AAA62126 753 aa linear PRI 08-FEB-1995
 DEFINITION AMP deaminase isoform L splicing variant.
 ACCESSION AAA62126
 PID g644509
 VERSION AAA62126.1 GI:644509
 DBSOURCE locus HUMAMPD2 accession M91029.1
 KEYWORDS .
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (residues 1 to 753)
 AUTHORS Van den Bergh, F. and Sabina, R.L.
 TITLE Exon shuffling at the 5' end of the human AMPD2 gene produces
 multiple transcripts encoding variable N-terminal extensions of
 isoform L
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 753)
 AUTHORS Sabina, R.L.
 TITLE Direct Submission
 JOURNAL Submitted (06-OCT-1994) Richard L Sabina, Biochemistry, Medical
 College of Wisconsin, 8701, Watertown Plank Road, Milwaukee,
 Wisconsin, 53226, USA
 COMMENT Method: conceptual translation.
 FEATURES
 source Location/Qualifiers
 1..753
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /cell_type="T-lymphoblast"
 /tissue_type="placenta fetal heart"
 Protein 1..753
 /product="AMP deaminase isoform L splicing variant"
 /EC_number="3.5.4.6"
 CDS 1..753
 /gene="AMPD2"
 /coded_by="join(M91029.1:<1..7,M91029.1:236..2491)"
 ORIGIN
 1 aeelftrsla eselrsapye fpeespieql eerrqrlerq isqdvklepd illrakqdf1
 61 ktdsdsdlql ykeggqgd rslrerdvle refqrvtisg eekcgvpftd lldaaksvvr
 121 alfirekyma lslqsfcptt rrylqqlaek plettryeqg pdtpvsadap vhppaleqhp
 181 yehcepstmp gdlglglrmv rgvvhvytrr epdehcseve lypdqlgefz adnvlmali
 241 ingpiksfcy rrlqylsskf qmhvllnemk elaaqkkvph rdfynirkvd thihasscmn
 301 qkhlrfikr amkrhleeiv hveggreqtl revfesmlt aydlsvdtld vhadrtfhr
 361 fdkfnakynp igesvlreif iktdnrsvsgk yfahiikevm sdleeskyqn aelrlsiygr
 421 srdewdklar wavmhrvhsp nvrwlvqvpr lfdvyrktgq lanfqemlen iflplfeatv
 481 hpashpelhl flehvdgfdv vddeskenh vfnlesplpe awveednppy ayylyytfan
 541 mamlnhlrrq rgfhtfvlrp hcgeagpihh lvsafmlaen ishglrrka pvlqlyyla
 601 qigiamspls nnsflsyhr nplpeylsrg lmvslstddp lqfhftkepl meeysiatqv

661 wklsscdmce larnsvlmsg fshkvkshwl gpnytkegpe gndirrtntp dirvgryet
721 lcqelalitq avqsemleti peeagitmsp gpq

//

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☐ 1: AAD03459. contains similari...[gi:4115949] Nucleotide, Related Sequences, Taxonomy, BLink, LinkOut

LOCUS AAD03459 275 aa linear PLN 10-AUG-1999
 DEFINITION contains similarity to adenosine deaminases [Arabidopsis thaliana].
 ACCESSION AAD03459
 PID g4115949
 VERSION AAD03459.1 GI:4115949
 DBSOURCE locus T4B21 accession [AF118223.2](#)
 KEYWORDS .
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (residues 1 to 275)
 AUTHORS Abbott,A., Kock,J. and Lehnert,L.
 TITLE The sequence of A. thaliana T4B21
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 275)
 AUTHORS Washington University Genome Sequencing Center.
 TITLE The A. thaliana Genome Sequencing Project
 JOURNAL Unpublished
 REFERENCE 3 (residues 1 to 275)
 AUTHORS Waterston,R.
 TITLE Direct Submission
 JOURNAL Submitted (06-JAN-1999) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 REFERENCE 4 (residues 1 to 275)
 AUTHORS Waterston,R.
 TITLE Direct Submission
 JOURNAL Submitted (06-AUG-1999) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 REFERENCE 5 (residues 1 to 275)
 AUTHORS Waterston,R.
 TITLE Direct Submission
 JOURNAL Submitted (10-AUG-1999) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 COMMENT Method: conceptual translation.
 FEATURES
 source
 1..275
 /organism="Arabidopsis thaliana"
 /cultivar="Columbia"
 /db_xref="taxon:3702"
 /chromosome="IV"
 /map="unknown"
 /clone="T4B21"
 Protein
 1..275
 /name="contains similarity to adenosine deaminases"
 CDS
 1..275
 /gene="T4B21.20"
 /coded_by="complement(join(AF118223.2:80842..80913,

AF118223.2:80994..81107,AF118223.2:81196..81265,
AF118223.2:81344..81720,AF118223.2:81791..81850,
AF118223.2:82153..82210,AF118223.2:82365..82441)) "

ORIGIN

```
1 mewiqslpki elhahlngsi rdstllelar vlgekgvivf advehvvedf alenvvylel
61 rttpkrsdsi gmskrsymea viqglrsvse vdidfvtsd sqklhnagd igrkkiyvrl
121 llsidrrett esametsvsvs kqakllrilk rlmqktfdtl lfslkvklal emrdvgvvgi
181 dlsgnplvge wstflpalqy akdndlhitl hcgevpnpke iqamldfkph righacffkd
241 edwtklksfr ipveicltsn ivtksissid ihhfg
```

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☐ 1: 1002274A[gi:351916]

LOCUS 351916 105 aa linear VRT 20-JUN-1996
DEFINITION cytochrome c.
ACCESSION 351916
PID g351916
VERSION GI:351916
DBSOURCE prf: locus 1002274A;
state: myeloma/lymphoma;
taxonomy: Aves.
KEYWORDS Cytochrome c Gene Allele; Chicken; Genomic Blot Hybridization; Seq
Determination; 104AAs; 1600bp; Limited Polymorphism; 1 Enz in
Chicken Genome.
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Archosauria; Aves; Neognathae; Galliformes;
Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (residues 1 to 105)
AUTHORS Limbach, K.J. and Wu, R.
TITLE Isolation and characterization of two alleles of the chicken
cytochrome c gene
JOURNAL Nucleic Acids Res. 11 (24), 8931-8950 (1983)
MEDLINE 84169527
COMMENT gene CC9/CC10.
FEATURES Location/Qualifiers
source 1..105
/organism="Gallus gallus"
/db_xref="taxon:9031"
ORIGIN
1 mgdiekgkki fvqkcsqcht vekggkhktg pnhglfgrk tgqaegfsyt danknkgitw
61 gedtlmeyle npkkyipgtk mifagikkks ervdliaylk datsk
//

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☐ 1: P22333. ADENOSINE DEAMINA...
[gi:2506342]

Related Sequences, PubMed, Taxonomy, BLINK,
LinkOut

LOCUS ADD_ECOLI 333 aa linear BCT 20-AUG-2001
 DEFINITION ADENOSINE DEAMINASE (ADENOSINE AMINOHYDROLASE).
 ACCESSION P22333
 PID g2506342
 VERSION P22333 GI:2506342
 DBSOURCE swissprot: locus ADD_ECOLI, accession P22333;
 class: standard.
 extra accessions: P78240, P78163, created: Aug 1, 1991.
 sequence updated: Nov 1, 1997.
 annotation updated: Aug 20, 2001.
 xrefs: gi: gi: [145200](#), gi: gi: [145201](#), gi: gi: [2367121](#), gi: gi:
[1787910](#), gi: gi: [1742665](#), gi: gi: [1742677](#), gi: gi: [1742679](#), gi: gi:
[1742685](#), gi: gi: [1742692](#), gi: gi: [1742693](#), gi: gi: [1742711](#), gi: gi:
[1742717](#), gi: gi: [95641](#)
 xrefs (non-sequence databases): HSSP P03958, EcoGene EG10030,
 InterPro IPR001365, Pfam PF00962, PROSITE PS00485
 KEYWORDS Hydrolase; Nucleotide metabolism; Complete proteome.
 SOURCE Escherichia coli.
 ORGANISM Escherichia coli
 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 Escherichia.
 REFERENCE 1 (residues 1 to 333)
 AUTHORS Chang, Z.Y., Nygaard, P., Chinault, A.C. and Kellems, R.E.
 TITLE Deduced amino acid sequence of Escherichia coli adenosine deaminase
 reveals evolutionarily conserved amino acid residues: implications
 for catalytic function
 JOURNAL Biochemistry 30 (8), 2273-2280 (1991)
 MEDLINE [91152042](#)
 REMARK SEQUENCE FROM N.A.
 STRAIN=K12
 REFERENCE 2 (residues 1 to 333)
 AUTHORS Blattner, F.R., Plunkett, G.I.I.I., Bloch, C.A., Perna, N.T.,
 Burland, V., Riley, M., Collado-Vides, J., Glasner, J.D., Rode, C.K.,
 Mayhew, G.F., Gregor, J., Davis, N.W., Kirkpatrick, H.A., Goeden, M.A.,
 Rose, D.J., Mau, B. and Shao, Y.
 TITLE The complete genome sequence of Escherichia coli K-12
 JOURNAL Science 277 (5331), 1453-1474 (1997)
 MEDLINE [97426617](#)
 REMARK SEQUENCE FROM N.A.
 STRAIN=K12 / MG1655
 REFERENCE 3 (residues 1 to 333)
 AUTHORS Aiba, H., Baba, T., Fujita, K., Hayashi, K., Inada, T., Isono, K.,
 Itoh, T., Kasai, H., Kashimoto, K., Kimura, S., Kitakawa, M.,
 Kitagawa, M., Makino, K., Miki, T., Mizobuchi, K., Mori, H., Mori, T.,
 Motomura, K., Nakade, S., Nakamura, Y., Nashimoto, H., Nishio, Y.,
 Oshima, T., Saito, N., Sampei, G., Seki, Y., Sivasundaram, S.,
 Tagami, H., Takeda, J., Takemoto, K., Takeuchi, Y., Wada, C.,
 Yamamoto, Y. and Horiuchi, T.

TITLE A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map
JOURNAL DNA Res. 3 (6), 363-377 (1996)
MEDLINE 97251357
REMARK SEQUENCE FROM N.A.
STRAIN=K12
COMMENT On Oct 9, 1997 this sequence version replaced gi:113347.

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collaboration between the Swiss Institute of Bioinformatics and
the EMBL outstation - the European Bioinformatics Institute.
The original entry is available from <http://www.expasy.ch/sprot>
and <http://www.ebi.ac.uk/sprot>

[CATALYTIC ACTIVITY] ADENOSINE + H(2)O = INOSINE + NH(3) (ALSO ACTS
ON DEOXYADENOSINE).

[SIMILARITY] BELONGS TO THE ADENOSINE AND AMP DEAMINASES FAMILY.

FEATURES
 source Location/Qualifiers
 1..333
 /organism="Escherichia coli"
 /db_xref="taxon:562"
 1..333
 Protein 1..333
 /product="ADENOSINE DEAMINASE"
 /EC_number="3.5.4.4"
 Region 145
 /region_name="Conflict"
 /note="MISSING (IN REF. 1)."
 Site 197
 /site_type="active"
 /note="POTENTIAL."
 Site 245
 /site_type="active"
 /note="POTENTIAL."
 Site 278
 /site_type="active"
 /note="POTENTIAL."
 Site 279
 /site_type="active"
 /note="POTENTIAL."

ORIGIN
 1 midttlpltd ihrhldgnir pqtilelgrq ynislpaqsl etliphvqvi anepdlvsfl
 61 tkldwgvkvl asldacrrva feniedaarh glhyvelrfs pgymamahql pvagvveavi
 121 dgvgregcrtf gvqakligim srtfgeaacq qeleafahr dqitaldlag delgfpqslf
 181 lshfnrarda gwhitvhage aagpesiwqa irelgaerig hgvkaiedra lmdflaeqqi
 241 giescltsni qtstvaela hplktflehg irasintddp gvqgvdiie ytvaapaagl
 301 sreqirqaqi nglemaflsa eekralrekv aak
//

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